We claim:

1. A pharmaceutical composition for the treatment or prophylaxis of gastrointestinal disorders, comprising a diaminoalkyl compound and a pharmaceutically acceptable carrier.

2. The composition of claim 1, wherein the diaminoalkyl compound is cadaverine.

3. The composition of claim 1, wherein the diaminoalkyl compound is putrescine.

4. The composition of claim 1, wherein the gastrointestinal disorders result from an infection by an organism selected from the group consisting of *Shigella* spp., enteropathogenic *E. coli*, enterohemorrhagic *E. coli*, enterotoxigenic *E. coli*, enteroaggregative *E. coli*, uropathogenic *E. coli*, enteroinvasive *E. coli*, meningitis-causing *E. coli* K-1, *Yersinia pestis*, *Yersinia pseudotuberculosis*, *Yersinia enterocolitica*, *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium avium*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Listeria monocytogenes*, *Vibrio cholerae*, *Streptococcus pyogenes*, *Campylobacter jejuni*, *Bacteroides fragilis* and *Haemophilus influenzae*.

5. A method of using the pharmaceutical composition of claim 1, wherein the composition is administered to a host in an amount sufficient to prevent or to treat gastrointestinal disorders.

6. A method of treating or preventing gastrointestinal disorders, comprising the steps of administering an effective amount of cadaverine with a pharmaceutically acceptable carrier to a mammal suffering from, or at risk for, a gastrointestinal disorder.

7. The method of claim 6, wherein the mammal is a human.

8. The method of claim 6, wherein the gastrointestinal disorders result from an infection by *Shigella* spp.

9. A vaccine comprising

a pathogenic bacteria modified by the introduction of DNA that encodes lysine decarboxylase.

10. The vaccine of claim 9, wherein the pathogenic bacteria is selected from the group consisting of *Shigella* spp., enteropathogenic *E. coli*, enterohemorrhagic *E. coli*, enterotoxigenic *E. coli*, enteroaggregative *E. coli*, uropathogenic *E. coli*, enteroinvasive *E. coli*, meningitis-causing *E. coli* K-1, *Yersinia pestis*, *Yersinia pseudotuberculosis*, *Yersinia enterocolitica*, *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium avium*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Listeria monocytogenes*, *Vibrio cholerae*, *Streptococcus pyogenes*, *Campylobacter jejuni*, *Bacteroides fragilis* and *Haemophilus influenzae*.

11. The vaccine of claim 10, wherein the pathogenic bacteria is *Shigella* spp.

12. The vaccine of claim 9, wherein the vaccine is in a formulation selected from the group consisting of live attenuated bacteria, killed bacteria, bacterial components, conjugate vaccines, proteosome vaccines, and nucleoprotein (ribosomal) vaccines.

13. The vaccine of claim 9, wherein the DNA that encodes lysine decarboxylase is selected from the group consisting of *speC*, *ldc*, and *cadA*.

14. The vaccine of claim 13 wherein the DNA that encodes lysine decarboxylase is the *cadA* gene or portions thereof.

15. The vaccine of claim 9, wherein the vaccine is further modified by the insertion of at least one additional gene or portion thereof.

16. The vaccine of claim 15, wherein the additional gene or portion thereof is selected from the group consisting of DNA which codes for HIV antigen, influenza A virus nucleoprotein, influenza A

virus hemagglutinin, measles virus nucleoprotein, measles virus hemagglutinin, *Mycobacterium tuberculosis* secreted proteins, hantavirus glycoproteins, and nucleocapsid proteins.

17. A vaccine wherein the enterotoxin produced by a pathogenic bacteria is attenuated, comprising a diaminoalkyl compound and a vaccine based on the pathogenic bacteria.

18. The vaccine of claim 17, wherein the pathogenic bacteria is selected from the group consisting of *Shigella* spp., enteropathogenic *E. coli*, enterohemorrhagic *E. coli*, enterotoxigenic *E. coli*, enteroaggregative *E. coli*, uropathogenic *E. coli*, enteroinvasive *E. coli*, meningitis-causing *E. coli* K-1, *Yersinia pestis*, *Yersinia pseudotuberculosis*, *Yersinia enterocolitica*, *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium avium*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Listeria monocytogenes*, *Vibrio cholerae*, *Streptococcus pyogenes*, *Campylobacter jejuni*, *Bacteroides fragilis* and *Haemophilus influenzae*.

19. The vaccine of claim 18, wherein the pathogenic bacteria is *Shigella* spp.

20. The vaccine of claim 17, wherein the vaccine is in a formulation selected from the group consisting of live attenuated bacteria, killed bacteria, bacterial components, conjugate vaccines, proteosome vaccines, and nucleoprotein (ribosomal) vaccines.

21. A method for identifying bacterial genes which are incompatible with bacterial pathogenicity, comprising the steps of:

a. identifying a pair of closely related bacterial species where one species is pathogenic, and the other is non-pathogenic;

b. comparing the genomes of said bacterial species pair;

c. determining at least one genetic locus which is present in the non-pathogenic species but is absent in the pathogenic species;

d. identifying at least one gene in the genetic locus that is present in the non-pathogenic bacteria but is absent or non-functional in the pathogenic bacteria; and

e. confirming that the expression of the gene attenuates the pathogenicity of said pathogenic bacteria.

22. The method of claim 21 wherein the bacterial gene which is present in the non-pathogenic bacteria but absent or non-functional in the pathogenic bacteria is an "anti-virulence" gene.

23. The method of claim 21, wherein the gene present in the non-pathogenic bacteria encodes lysine decarboxylase (LDC).

24. The method of claim 23, wherein the gene present is selected from the group consisting of *speC*, *ldc*, and *cadA*.

25. The method of claim 21, wherein the pathogenic bacteria is *Shigella* spp.

26. The method of claim 21, wherein the gene present in the non-pathogenic bacteria is at least one of *nadA* or *nadB*.

27. A method of identifying new pharmaceuticals for the treatment of bacterial pathogenesis, comprising the steps of:

a. identifying a pair of closely related bacterial species where one species is pathogenic and the other is non-pathogenic;

b. comparing the genomes of said bacterial species pair;

c. determining at least one genetic locus which is present in the non-pathogenic species but is absent in the pathogenic species;

d. identifying at least one gene in the genetic locus that is present in the non-pathogenic bacteria but is absent or non-functional in the pathogenic bacteria;

e. identifying at least one gene product of the gene; and

f. confirming that said gene product, or a compound resulting from the enzymatic activity of said gene product, attenuates the pathogenicity of said pathogenic bacteria.

28. The method of claim 27, wherein the gene present in the non-pathogenic bacteria but absent in the pathogenic bacteria is an "anti-virulence" gene.

29. The method of claim 27, wherein the bacterial pathogenesis is gastrointestinal.

30. A method for treating bacterial pathogenesis, comprising administering to a patient in need thereof an effective amount of the gene product, or of a compound resulting from the enzymatic activity of said gene product, identified by the process of claim 27.

31. The method of claim 29, wherein the bacterial pathogenesis is caused by *Shigella* spp.

32. A method for designing a vaccine directed to a pathogenic bacteria, comprising insertion of the "anti-virulence" gene identified by the process of claim 22 into the genome of the pathogenic bacterium; and using said bacterium in a vaccine.

33. The method of claim 27, wherein the pathogenic bacteria is selected from the group consisting of *Shigella* spp., enteropathogenic *E. coli*, enterohemorrhagic *E. coli*, enterotoxigenic *E. coli*, enteroaggregative *E. coli*, uropathogenic *E. coli*, enteroinvasive *E. coli*, meningitis-causing *E. coli* K-1, *Yersinia pestis*, *Yersinia pseudotuberculosis*, *Yersinia enterocolitica*, *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium avium*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Listeria monocytogenes*, *Vibrio cholerae*, *Streptococcus pyogenes*, *Campylobacter jejuni*, *Bacteroides fragilis* and *Haemophilus influenzae*.

34. The method of claim 27, wherein the vaccine is further modified by the insertion of at least one additional gene or portion thereof.

35. The method of claim 34, wherein the additional gene or portion thereof is selected from the group consisting of DNA which codes for HIV antigen, influenza A virus nucleoprotein, influenza A virus hemagglutinin, measles virus nucleoprotein, measles virus hemagglutinin, *Mycobacterium tuberculosis* secreted proteins, hantavirus glycoproteins and nucleocapsid proteins.

36. A pharmaceutical composition for the treatment or prophylaxis of gastrointestinal disorders, comprising quinolinate and a pharmaceutically acceptable carrier.

37. The composition of claim 36, wherein the gastrointestinal disorders result from an infection by *Shigella* spp.

38. A method of using the pharmaceutical composition of claim 36, wherein the composition is administered to a host in an amount sufficient to prevent or to treat gastrointestinal disorders.

39. A method of treating or preventing gastrointestinal disorders, comprising the steps of administering an effective amount of quinolinate with a pharmaceutically acceptable carrier to a mammal suffering from, or at risk for, a gastrointestinal disorder.

40. The method of claim 39, wherein the mammal is a human.

41. The composition according to claim 4, wherein the gastrointestinal disorders result from an infection by *Shigella* spp.

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